AMENDMENTS TO THE CLAIMS

This listing of the claims replaces all prior listings and versions:

1. (withdrawn) An isolated, non-canonical zinc finger binding protein encoded by the polynucleotide of claim 30.

2-22. (canceled)

23. (withdrawn) The isolated polynucleotide of claim 30, wherein the target sequence is in an animal cell.

24. (withdrawn) The isolated polynucleotide of claim 23, wherein the target sequence is in a human cell.

25. (previously presented) The isolated polynucleotide of claim 30, wherein the target sequence is a promoter sequence.

26. (previously presented) The isolated polynucleotide of claim 30, wherein the zinc finger binding protein comprises three zinc finger components.

27. (previously presented) The isolated polynucleotide of claim 30, wherein the target sequence comprises about 9 to about 14 contiguous base pairs.

28. (previously presented) The isolated polynucleotide of claim 26, wherein the third zinc finger component comprises a non-canonical zinc finger component.

29. (cancelled)

30. (currently amended) An isolated polynucleotide encoding a non-naturally-occurring zinc-finger binding protein comprising a non-canonical zinc finger component, wherein:

(i) said non-canonical zinc finger component contains a beta turn comprising two amino-terminal zinc coordinating cysteine or histidine residues and an alpha helix comprising two carboxy-terminal zinc coordinating cysteine or histidine residues, wherein at least one of the ~~amino-terminal~~ zinc coordinating residues is a histidine residue ~~or~~ and at least one of the ~~carboxy-terminal~~ zinc coordinating residues is a cysteine residue ~~and further wherein at least one of the zinc coordinating residues is a histidine residue~~;

(ii) the non-canonical zinc finger component comprises 1, 2, 3, 4, 6 or 7 amino acids between the two carboxy-terminal zinc coordinating residues and 2, 3 or 4 amino acids between the two amino-terminal zinc coordinating residues; and

(iii) the non-canonical ~~recognition region of~~ zinc-finger binding domain protein comprises a recognition helix of at least 7 amino acids in length, wherein the recognition helix is non-naturally occurring and is engineered to bind to a target nucleic acid sequence in a plant cell.

31. (original) An expression vector comprising the polynucleotide of claim 30.

32. (previously presented) An isolated host cell comprising the polynucleotide of claim 30.

33. (withdrawn) A fusion polypeptide comprising: (a) an isolated zinc finger binding protein according to claim 1 and (b) at least one functional domain.

34. (withdrawn) The polynucleotide of claim 39, wherein the functional domain is a repressive domain.

35. (withdrawn) The polynucleotide of claim 34, wherein the repressive domain is selected from the group consisting of KRAB, MBD-2B, v-ErbA, MBD3, TR and members of the DNMT family.

36. (previously presented) The polynucleotide of claim 39, wherein the functional domain is an activation domain.

37. (previously presented) The polynucleotide of claim 36, wherein the activation domain is selected from the group consisting of maize C1, VP16, p65 subunit of NF-kappa B, and VP64.

38. (withdrawn) The polynucleotide of claim 39, wherein the functional domain is an endonuclease.

39. (previously presented) An isolated polynucleotide according to claim 30 further encoding a functional domain.

40. (original) An expression vector comprising the polynucleotide of claim 39.

41. (previously presented) An isolated host cell comprising the polynucleotide of claim 39.

42. (withdrawn) A method of modulating expression of a gene in a plant cell, the method comprising the step of contacting a cell with a polynucleotide according to claim 39.

43. (withdrawn) The method of claim 42, wherein the zinc finger binding protein binds to a target site in a gene encoding a product selected from the group consisting of gamma-tocopherol methyl transferase (GMT), vascular endothelial growth factor, erythropoietin, androgen receptor, PPAR-γ2, p16, p53, pRb, dystrophin and e-cadherin.

44. (withdrawn) The method of claim 42, wherein the functional domain comprises a repressive domain.

45. (withdrawn) The method of claim 44, wherein the repressive domain is selected from the group consisting of KRAB, MBD-2B, v-ErbA, MBD3, TR and members of the DNMT family.

46. (withdrawn) The method of claim 42, wherein the functional domain comprises an activation domain.

47. (withdrawn) The method of claim 46, wherein the activation domain is selected from the group consisting of maize C1, VP16, p65 subunit of NF-kappa B, and VP64.

48. (withdrawn) The method of claim 42, wherein the functional domain is an endonuclease.

49 to 51. (canceled).

52. (withdrawn) A composition comprising a non-naturally-occurring zinc-finger binding protein according to claim 1 and a pharmaceutically acceptable excipient.

53. (previously presented) A composition comprising a polynucleotide according to claim 39 and a pharmaceutically acceptable excipient.

54. (previously presented) The isolated polynucleotide of claim 26, wherein the first zinc finger component comprises a non-canonical zinc finger component.

55. (previously presented) The isolated polynucleotide of claim 30, wherein the zinc finger binding protein comprises four zinc finger components.

56. (currently amended) An isolated polynucleotide encoding a non-naturally occurring zinc-finger binding protein comprising a non-canonical zinc finger component, wherein:

(i) said non-canonical zinc finger component contains a beta turn comprising two amino-terminal zinc coordinating cysteine ~~or histidine residues~~ and an alpha helix comprising two carboxy-terminal zinc coordinating cysteine or histidine residues, wherein ~~the two amino-terminal zinc coordinating residues are cysteine residues,~~ one of the carboxy-terminal zinc coordinating residues is a histidine residue and one of the carboxy-terminal zinc coordinating residues is a cysteine residue;

(ii) the non-canonical zinc finger component comprises 2 amino acids between the two amino-terminal zinc coordinating cysteine residues; and

(iii) the protein comprises a non-naturally occurring recognition helix that is engineered to bind to a target nucleic acid sequence.

57. (previously presented) The polynucleotide of claim 56, wherein the carboxy-terminal zinc coordinating histidine residue is amino terminal to the carboxy-terminal zinc coordinating cysteine residue.

58 to 61. (cancelled).